

**AMENDMENTS TO THE CLAIMS**

1. **(Currently Amended)** A method of identifying bacteria, comprising:

a) providing:

- i) amplified random genomic sequences from a plurality of bacterial species, wherein said amplified genomic sequences range between 1 – 2 kb and are arrayed on a solid support so as to create a plurality of arrayed elements, and wherein the nucleotide sequence of said amplified genomic sequences comprises unknown sequences,
- ii) labeled target DNA from a test bacteria of interest, wherein said labeled target DNA is labeled with a first fluorescent dye, and
- iii) labeled reference DNA from at least four strains of reference bacteria, wherein said reference bacteria are members of the group consisting of said plurality of bacterial species, wherein said labeled reference DNA is labeled with a second fluorescent dye[[: and]],

- b) hybridizing said target DNA and said reference DNA to said amplified genomic sequences having unknown sequences on said plurality of arrayed elements, wherein each hybridized target DNA has a fluorescent target signal, and each hybridized reference DNA has a fluorescent reference signal,
- c) determining the presence of 70% homology between said hybridized target DNA and one or more of said reference DNA by comparing said fluorescent target signal with said fluorescent reference signal, and
- d) identifying, without the need for sequencing said amplified genomic sequences, the species of said test bacteria based on said homology.

2. **(Original)** The method of claim 1, wherein said test bacteria are from a sample obtained from a subject.

3. **(Previously Presented)** The method of claim 1, wherein said test bacteria are

pathogenic.

4. **(Original)** The method of claim 1, wherein said test bacteria are environmental isolates.

5. **(Original)** The method of claim 1, wherein said solid support is a microchip.

6. **(Previously Presented)** The method of claim 26, wherein said calculating comprises statistical analysis.

7. **(Canceled)**

8. **(Original)** The method of claim 1, further comprising the step of producing hybridization profiles of said test and reference bacteria.

9. **(Currently Amended)** A method of identifying bacteria, comprising:

- a) providing:
  - i) amplified random genomic sequences from a plurality of bacterial species, wherein said amplified genomic sequences range between 1 – 2 kb and are arrayed on at least one microchip, so as to create a plurality of arrayed elements, and wherein the nucleotide sequence of said amplified genomic sequences comprises unknown sequences,
  - ii) labeled target DNA from a test bacteria of interest, wherein said labeled target DNA is labeled with a first fluorescent dye, and
  - iii) labeled reference DNA from at least four strains of reference bacteria, wherein said reference bacteria are members of the group consisting of said plurality of bacterial species, wherein said labeled target DNA is labeled with a second fluorescent dye[[: and]],

- b) hybridizing said target DNA and said reference DNA to said amplified genomic sequences having unknown sequences on said plurality of arrayed elements, wherein each hybridized target DNA has a fluorescent target signal, and each hybridized reference DNA has a fluorescent reference signal, and
- c) determining the presence of 70% homology between said hybridized target DNA and one or more of said reference DNA by comparing said fluorescent target signal with said fluorescent reference signal, and
- d) identifying, without the need for sequencing said amplified genomic sequences, the species of said test bacteria based on said homology.

10. **(Original)** The method of claim 9, wherein said test bacteria are from a sample obtained from a subject.

11. **(Previously Presented)** The method of claim 10, wherein said test bacteria are pathogenic.

12. **(Original)** The method of claim 9, wherein said test bacteria are environmental isolates.

13. **(Original)** The method of claim 9, further comprising the step of producing hybridization profiles of said test and reference bacteria.

14. **(Previously Presented)** The method of claim 27, wherein said calculating comprises statistical analysis.

15-21. **(Canceled)**

22. **(Previously Presented)** The method of Claim 1, wherein said solid support comprises at least 60 arrayed elements.

23. **(Previously Presented)** The method of Claim 1, wherein said solid support comprises at least 96 arrayed elements.

24. **(Previously Presented)** The method of Claim 9, wherein said solid support comprises at least 60 arrayed elements.

25. **(Previously Presented)** The method of Claim 9, wherein said solid support comprises at least 96 arrayed elements.

26. **(Previously Presented)** The method of Claim 1, further comprising calculating a ratio of said fluorescent target signal to said fluorescent reference signal at each array element thereby determining the species of said test bacteria.

27. **(Previously Presented)** The method of Claim 9, further comprising calculating a ratio of said fluorescent target signal to said fluorescent reference signal at each array element thereby determining the species of said test bacteria.